

FIGURE 1A

ATG AAG CCG TAC TTC TGC CGT GTC TTT GTC TTC TGC TTC CTA ATC	45
M K P Y F C R V F V F C F L I	
5 10 15	
AGA CTT TTA ACA GGA GAA ATC AAT GGC TCG GCC GAT CAT AGG ATG	90
R L L F G E I N G S A D H R M	
20 25 30	
TTT TCA TTT CAC AAT GGA GGT GTA CAG ATT TCT TGT AAA TAC CCT	135
F S F H N G G V Q I S C K Y P	
35 40 45	
GAG ACT GTC CAG CAG TTA AAA ATG CGA TTG TTC AGA GAG AGA GAA	180
E T V Q Q L K M R L F R E R E	
50 55 60	
GTC CTC TGC GAA CTC ACC AAG ACC AAG GGA AGC GGA AAT GCG GTG	225
V L C E L T K T K G S G N A V	
65 70 75	
TCC ATC AAG AAT CCA ATG CTC TGT CTA TAT CAT CTG TCA AAC AAC	270
S I K N P M L C L Y H L S N N	
80 85 90	
AGC GTC TCT TTT TTC CTA AAC AAC CCA GAC AGC TCC CAG GGA AGC	315
S V S F F L N N P D S S Q G S	
95 100 105	
TAT TAC TTC TGC AGC CTG TCC ATT TTT GAC CCA CCT CCT TTT CAA	360
Y Y F C S L S I F D P P P F Q	
110 115 120	
GAA AGG AAC CTT AGT GGA GGA TAT TTG CAT ATT TAT GAA TCC CAG	405
E R N L S G G Y L H I Y E S Q	
125 130 135	
CTC TGC TGC CAG CTG AAG CTC TGG CTA CCC GTA GGG TGT GCA GCT	450
L C C Q L K L W L P V G C A A	
140 145 150	
TTC GTT GTG GTA CTC CTT TTT GGA TGC ATA CTT ATC ATC TGG TTT	495
F V V V L L F G C I L I I W F	
155 160 165	
TCA AAA AAG AAA TAC GGA TCC AGT GTG CAT GAC CCT AAT AGT GAA	540
S K K K Y G S S V H D P N S E	
170 175 180	
TAC ATG TTC ATG GCG GCA GTC AAC ACA AAC AAA AAG TCT AGA CTT	585
Y M F M A A V N T N K K S R L	
185 190 195	
GCA GGT GTG ACC TCA	600
A G V T S	
200	

FIGURE 1B

mCRP1	MKPYFCRVFV	FCFLIRLL--	-----TGEIN	GS----	ADHR	MFSFHNGGVQ	39
mCD28	MT-----	----LRLLFL	ALNFFSVQVT	ENKILVKQSP	LLVVDSEVS		38
Consensus	M.....RLL..V.		
mCRP1	ISCKYPETV-	-QQLKMRLFR	--EREV-LCE	LTKTKGSGNA	VSIKNPMLCL		34
mCD28	LSCRYSYNLL	AKEFRASLYK	GVNSDVEVCV	GNGNFTYQPQ	FRSNAEFNCD		33
Consensus	.SC.Y.....L..V..C.C.		
mCRP1	YHLSNNSVSF	FLNNDSSQG	SYFCSLSIF	DPPPFQERNL	SGGYL-HIYE		133
mCD28	GDFDNETVTF	RLWNLHVNHT	DIYFCKIEFM	YPPPYLDNER	SNGTIIHIKE		133
Consensus	...N..V.F	.L.N.....	..YFC.....	.PPP.....	S.G...HI.E		
mCRP1	SQLC---CQL	KL-W-LPVGC	AA-FVVLLF	GCIL-IIWFS	KKKY----GS		172
mCD28	KHLCHTQSSP	KLFWALVVVA	GVLFYGLLV	TVALCVIWTN	SRNRLLQVT		138
Consensus	..LC.....	KL.W.L.V..	...F...LL.	...L..IW..		
mCRP1	SVH-DPNSEY	MFMAAVNTNK	KSR-LAGVTS				200
mCD28	TMMTPTRRPG	LTRKPYQPYA	PARDFAAYRP				218
ConsensusP....R..A....			

FIGURE 2A

ATG CAG CTA AAG TGT CCC TGT TTT GTG TCC TTG GGA ACC AGG CAG	45
M Q L K C P C F V S L G T R Q	15
	5 10
CCT GTT TGG AAG AAG CTC CAT GTT TCT AGC GGG TTC TTT TCT GGT	90
P V W K K L H V S S G F F S G	30
	20 25 30
CTT GGT CTG TTC TTG CTG CTG TTG AGC AGC CTC TGT GCT GCC TCT	135
L G L F L L L L S S L C A A S	45
	35 40
GCA GAG ACT GAA GTC GGT GCA ATG GTG GGC AGC AAT GTG GTG CTC	180
A E T E V G A M V G S N V V L	60
	50 55
AGC TGC ATT GAC CCC CAC AGA CGC CAT TTC AAC TTG AGT GGT CTG	225
S C I D P H R R H F N L S G L	75
	65 70
TAT GTC TAT TGG CAA ATC GAA AAC CCA GAA GTT TCG GTG ACT TAC	270
Y V Y W Q I E N P E V S V T Y	90
	80 85
TAC CTG CCT TAC AAG TCT CCA GGG ATC AAT GTG GAC AGT TCC TAC	315
Y L P Y K S P G I N V D S S Y	105
	95 100
AAG AAC AGG GGC CAT CTG TCC CTG GAC TCC ATG AAG CAG GGT AAC	360
K N R G H L S L D S M K Q G N	120
	110 115
TTC TCT CTG TAC CTG AAG AAT GTC ACC CCT CAG GAT ACC CAG GAG	405
F S L Y L K N V T P Q D T Q E	135
	125 130
TTC ACA TGC CGG GTA TTT ATG AAT ACA GCC ACA GAG TTA GTC AAG	450
F T C R V F M N T A T E L V K	150
	140 145
ATC TTG GAA GAG GTG GTC AGG CTG CGT GTG GCA GCA AAC TTC AGT	495
I L E E V V R L R V A A N F S	165
	155 160
ACA CCT GTC ATC AGC ACC TCT GAT AGC TCC AAC CCG GGC CAG GAA	540
T P V I S T S D S S N P G Q E	180
	170 175
CGT ACC TAC ACC TGC ATG TCC AAG AAT GGC TAC CCA GAG CCC AAC	585
R T Y T C M S K N G Y P E P N	195
	185 190
CTG TAT TGG ATC AAC ACA ACG GAC AAT AGC CTA ATA GAC ACG GCT	630
L Y W I N T T D N S L I D T A	210
	200 205
CTG CAG AAT AAC ACT GTC TAC TTG AAC AAG TTG GGC CTG TAT GAT	675
L Q N N T V Y L N K L G L Y D	225
	215 220
GTA ATC AGC ACA TTA AGG CTC CCT TGG ACA TCT CGT GGC GAT GTT	720
V I S T L R L P W T S R G D V	240
	230 235

[illegible]

753
310
355
900
945
966

FIGURE 2B

mB7RP1	MQLKCPCFVS	LGTRQPVWKK	LHVSSGFFSG	LGLFLLLLLS-	SLCAASAETE	49
mCD80	MA--CNC--Q	LMQDTPL---	LKFPCPRII-	L-LFVLLIRL	SOVSSDVDEQ	41
Consensus	M...C.C...	L....P....	L.....	L.LF.LL...	S.....	
mB7RP1	VGAMVGSNVV	LSCIDPHRRH	FNLISGLVYW	QIENPEVSVT	YYLPYKSPGI	39
mCD80	LSKSVKDKVL	LPC-RYNSPH	EDESEDRIYW	QKHDKWV---	--LSVIAGKL	35
ConsensusV...V.	L.C.....H	...S....YW	Q.....V...	..L.....	
mB7RP1	NVDSSYKNRG	HLSLDSMKQG	NFSLYLKQVT	PQDTQEFTCR	VFMNTATELV	149
mCD80	KVWPEYKNR-	--TL--YDNT	TYSLIILGLV	LSDRGTYSKV	VQKKERGTYE	130
Consensus	.V...YKNR.	...L.....	..SL.....	..D.....C.	V.....	
mB7RP1	KILEEVVRLR	VAANFSTPVI	STSDSSNPGQ	ERTYTCMSKN	GYPEPNLYWI	199
mCD80	VKHLALVKLS	IKADFSTPNI	TESGNPSADT	KRI-TCFASG	GFPKPRFSWL	179
ConsensusV.L.	...A.FSTP.I	..S.....	.R..TC....	G.P.P...W.	
mB7RP1	-NTTDSLID	TALQNTVYL	NKLGLYDVIS	TLRLPWTSRG	DVLCCVENVA	248
mCD80	ENGRELPGIN	TTISQDPESE	LYTISSQLDF	NTTRNHTIKC	LIKYGDAHVS	229
Consensus	.N.....I.	T.....T...V.	
mB7RP1	LHQNITSISQ	AESFTGNNTK	NPQETHNNEL	KVLVPVLAVL	A-AAAFVSFI	297
mCD80	EDFTWEKPPE	DPPDSKNTLV	LFGAGFGAVI	TVVIVVVIK	CFCKHRSCFR	279
ConsensusN...V.V.V.....F.	
mB7RP1	IYRRTR-PHR	SYT-GPKTVQ	LELTDHA			322
mCD80	RNEASRETNN	SLTFGPPEAL	AEQTVFL			306
Consensus	...R....	S.T.GP...	.E.T...			

FIGURE 3A

ATG	CGG	CTG	GGC	AGT	CCT	GGA	CTG	CTC	TTC	CTG	CTC	TTC	AGC	AGC	45
M	R	L	G	S	P	G	L	L	F	L	L	F	S	S	
				5					10					15	
CTT	CGA	GCT	GAT	ACT	CAG	GAG	AAG	GAA	GTC	AGA	GCG	ATG	GTA	GGC	90
L	R	A	D	T	Q	E	K	E	V	R	A	M	V	G	
				20					25					30	
AGC	GAC	GTG	GAG	CTC	AGC	TGC	GCT	TGC	CCT	GAA	GGA	AGC	CGT	TTT	135
S	D	V	E	L	S	C	A	C	P	E	G	S	R	F	
				35					40					45	
GAT	TTA	AAT	GAT	GTT	TAC	GTA	TAT	TGG	CAA	ACC	AGT	GAG	TCG	AAA	180
D	L	N	D	V	Y	V	Y	W	Q	T	S	E	S	K	
				50					55					60	
ACC	GTG	GTG	ACC	TAC	CAC	ATC	CCA	CAG	AAC	AGC	TCC	TTG	GAA	AAC	225
T	V	V	T	Y	H	I	P	Q	N	S	S	L	E	N	
				65					70					75	
GTG	GAC	AGC	CGC	TAC	CGG	AAC	CGA	GCC	CTG	ATG	TCA	CCG	GCC	GGC	270
V	D	S	R	Y	R	N	R	A	L	M	S	P	A	G	
				80					85					90	
ATG	CTG	CGG	GGC	GAC	TTC	TCC	CTG	CGC	TTG	TTC	AAC	GTC	ACC	CCC	315
M	L	R	G	D	F	S	L	R	L	F	N	V	T	P	
				95					100					105	
CAG	GAC	GAG	CAG	AAG	TTT	CAC	TGC	CTG	GTG	TTG	AGC	CAA	TCC	CTG	360
Q	D	E	Q	K	F	H	C	L	V	L	S	Q	S	L	
				110					115					120	
GGA	TTC	CAG	GAG	GTT	TTG	AGC	GTT	GAG	GTT	ACA	CTG	CAT	GTG	GCA	405
G	F	Q	E	V	L	S	V	E	V	T	L	H	V	A	
				125					130					135	
GCA	AAC	TTC	AGC	GTG	CCC	GTC	GTC	AGC	GCC	CCC	CAC	AGC	CCC	TCC	450
A	N	F	S	V	P	V	V	S	A	P	H	S	P	S	
				140					145					150	
CAG	GAT	GAG	CTC	ACC	TTC	ACG	TGT	ACA	TCC	ATA	AAC	GGC	TAC	CCC	495
Q	D	E	L	T	F	T	C	T	S	I	N	G	Y	P	
				155					160					165	
AGG	CCC	AAC	GTG	TAC	TGG	ATC	AAT	AAG	ACG	GAC	AAC	AGC	CTG	CTG	540
R	P	N	V	Y	W	I	N	K	T	D	N	S	L	L	
				170					175					180	
GAC	CAG	GCT	CTG	CAG	AAT	GAC	ACC	GTC	TTC	TTG	AAC	ATG	CGG	GGC	585
D	Q	A	L	Q	N	D	T	V	F	L	N	M	R	G	
				185					190					195	
TTG	TAT	GAC	GTG	GTC	AGC	GTG	CTG	AGG	ATC	GCA	CGG	ACC	CCC	AGC	630
L	Y	D	V	V	S	V	L	R	I	A	R	T	P	S	
				200					205					210	
GTG	AAC	ATT	GGC	TGC	TGC	ATA	GAG	AAC	GTG	CTT	CTG	CAG	CAG	AAC	675
V	N	I	G	C	C	I	E	N	V	L	L	Q	Q	N	
				215					220					225	
CTG	ACT	GTC	GGC	AGC	CAG	ACA	GGA	AAT	GAC	ATC	GGA	GAG	AGA	GAC	720
L	T	V	G	S	Q	T	G	N	D	I	G	E	R	D	
				230					235					240	

[illegible]

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FIGURE 3B

hB7RP1	EKEVRAMVGS	DVELSCACPE	GSRFDLNDVY	VYWQTSESKT	VVTYHIPQNS	50
mB7RP1	ETEVGAMVGS	NVVLSCIDPH	RRHFNLSGLY	VYWQIENPEV	SVTYLPLPKS	50
Consensus	E.EV.AMVGS	.V.LSC..P.	..F.L...Y	VYWQ.....	.VTY..P..S	
hB7RP1	SLENVDSRYR	NRALMSPAGM	LRGDFSLRLF	NVTPQDEQKF	HCLVLSQ-SL	99
mB7RP1	PGINVDSSYK	NRGHLSLDSM	KQGNFSLYLK	NVTPQDTQEF	TCRVFMNTAT	100
Consensus	...NVDS.Y.	NR...S...M	..G.FSL.L.	NVTPQD.Q.F	.C.V.....	
hB7RP1	GFQEVLSVEV	TLHVAANFSV	PVVSAPHSPS	Q-DELTFTCT	SINGYPRPNV	143
mB7RP1	ELVKILEEVV	RLRVAANFST	PVISTSDSSN	PGQERTYTCM	SKNGYPEPNL	150
ConsensusL...V	.L.VAANFS.	PV.S...S..	...E.T.TC.	S.NGY.P.N.	
hB7RP1	YWINKTDNSL	LDQALQNDTV	FLNMRGLYDV	VSVLRIARTP	SVNIGCCIEI	199
mB7RP1	YWINTTDNSL	IDTALQNNTV	YLNKLGlyDV	ISTLRLPWTS	RGDVLCCEEN	200
Consensus	YWIN.TDNSL	.D.ALQN.TV	.LN..GLYDV	.S.LR...T.CC.EN	
hB7RP1	VLLQONLTVG	SQTGNDIGER	DKITENPVST	GEKNAATWSI	LAVLCLLVVV	248
mB7RP1	VALHQNITSI	SQAESFTGNN	TKNPQETHNN	ELKVLV--PV	LAVLAAAFV	248
Consensus	V.L.QN.T..	SQ...G...	.K....K...	..K...7...	LAVL...V	
hB7RP1	AVAIGWVCRD	RCLQHSYAG				267
mB7RP1	SFIIYR--RT	R-PHRSYTGP	KTVQLELTDH	A		276
Consensus	...I...R.	R...SY.G.			

Figure 4A

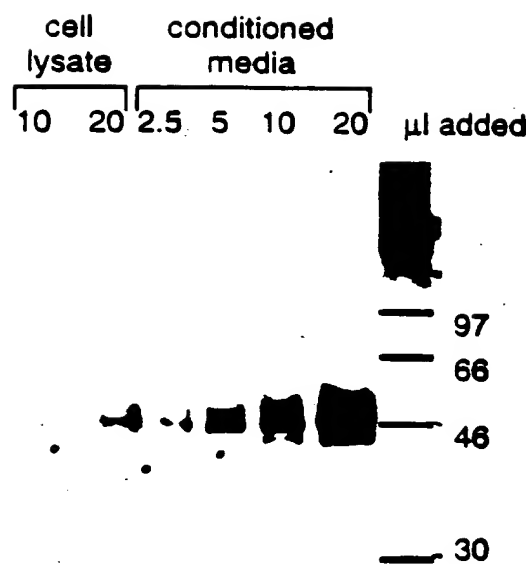


Figure 48

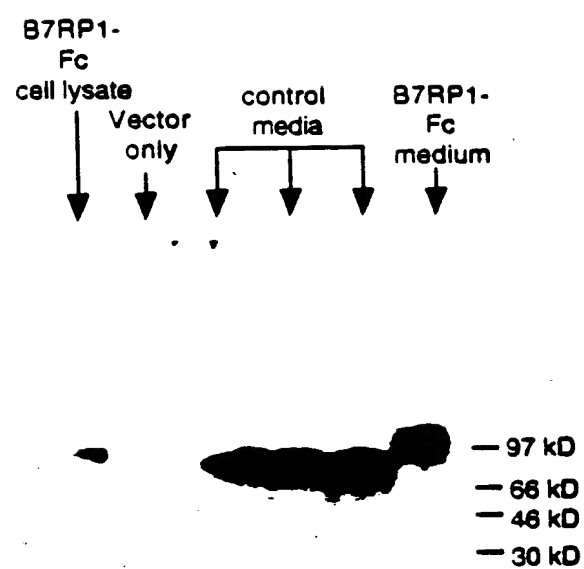


Figure 5

Fc fusion proteins

	Fc control	B7RP1	CRP1	B7.2	CTLA-4
Parental					
B7RP1					
CRP1					
hCD28					

Figure 6

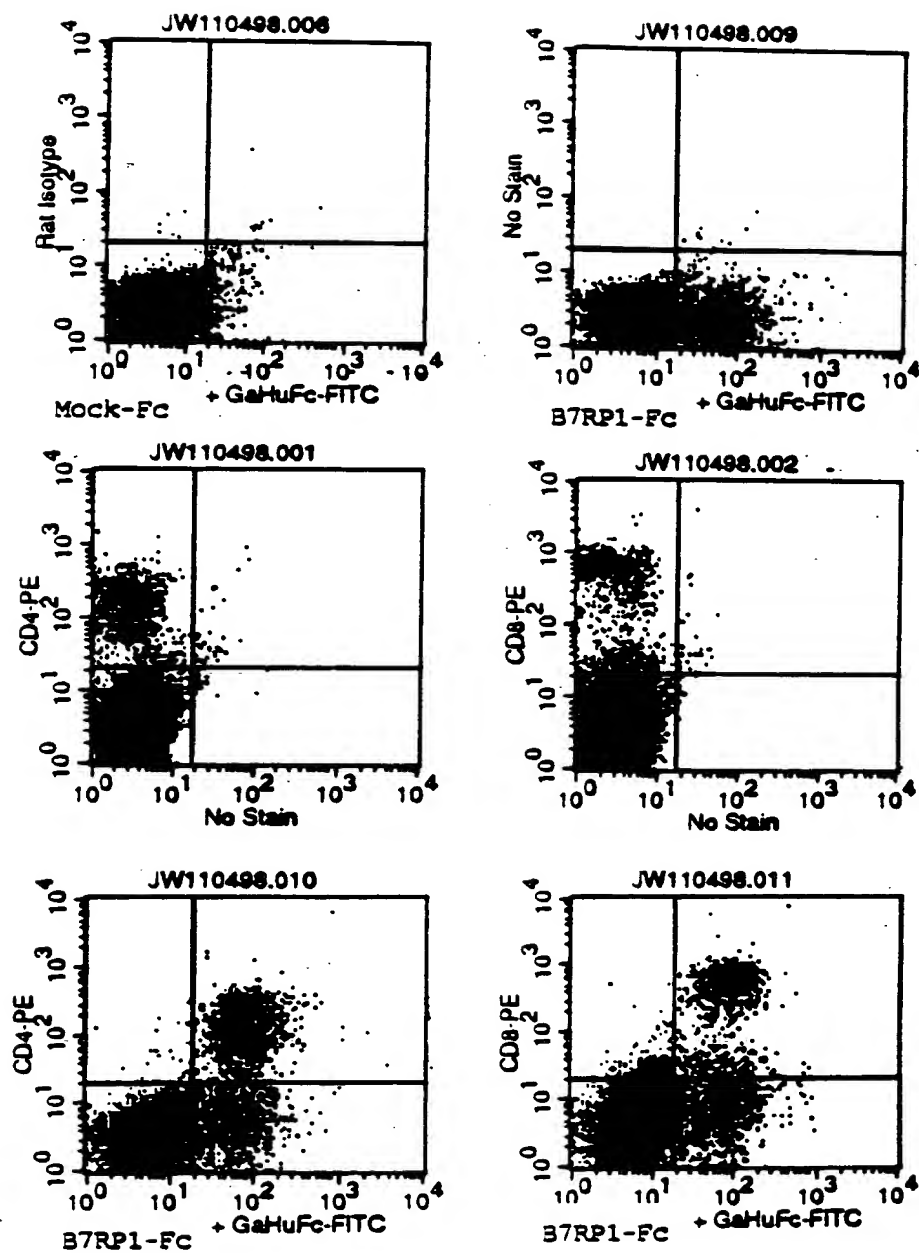


Figure 7

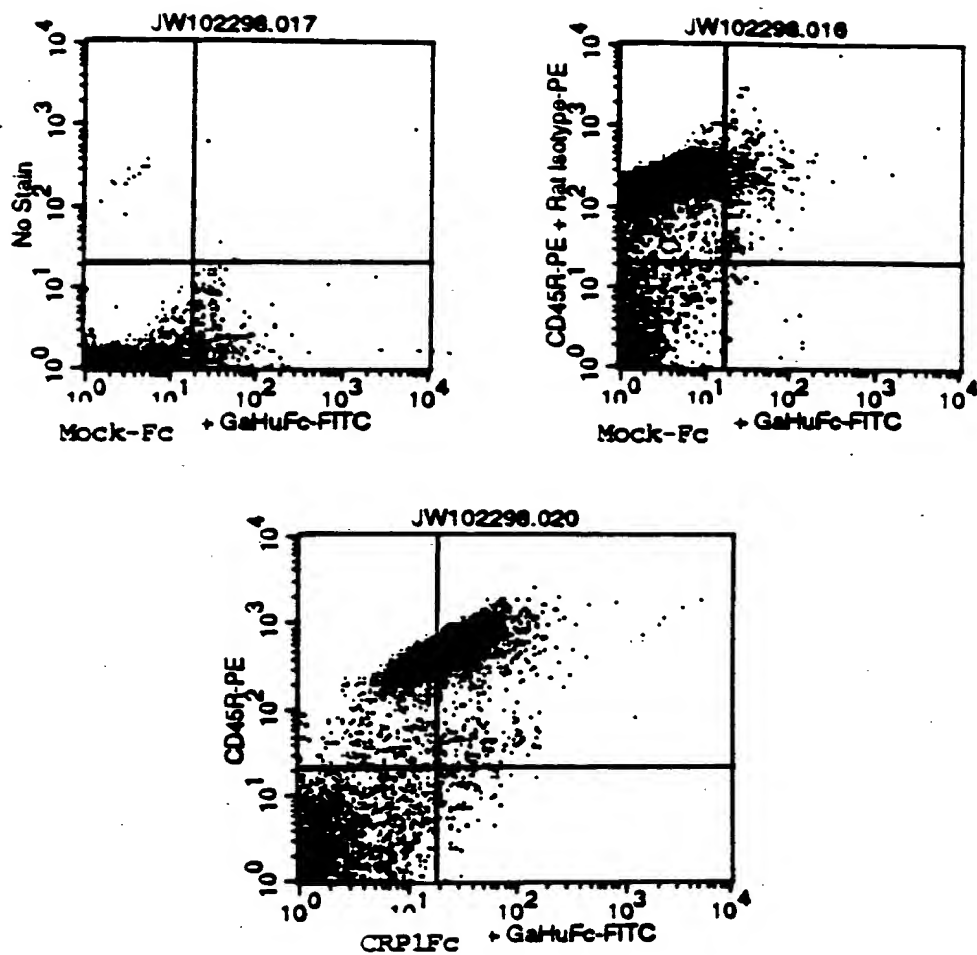


Figure 3

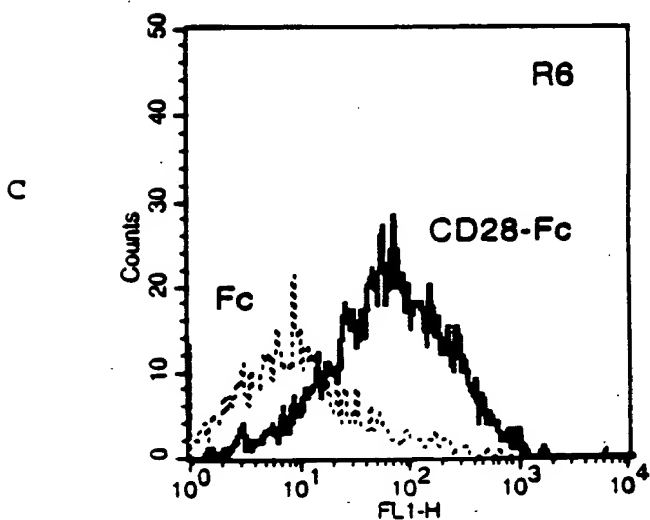
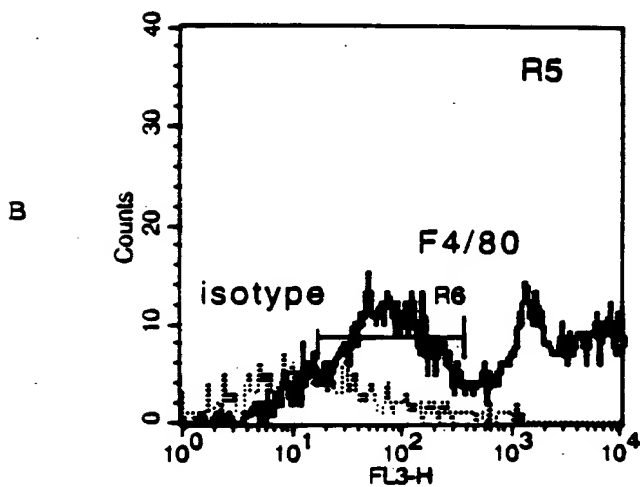
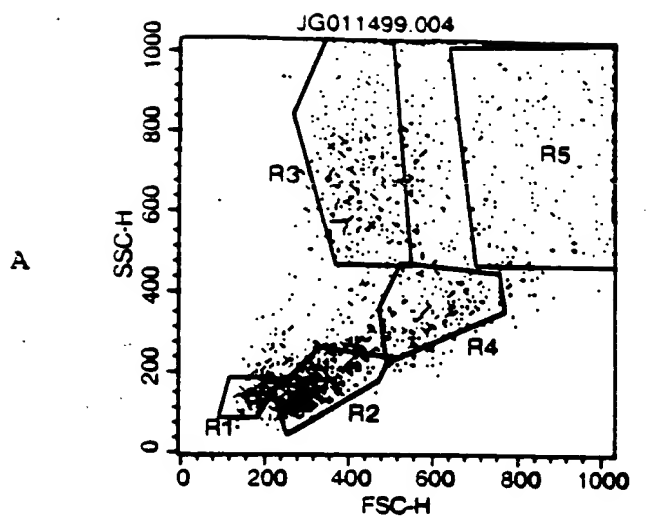


FIGURE 9

Con A stimulation of T-cells regulated
by B7RP1-Fc fusion protein

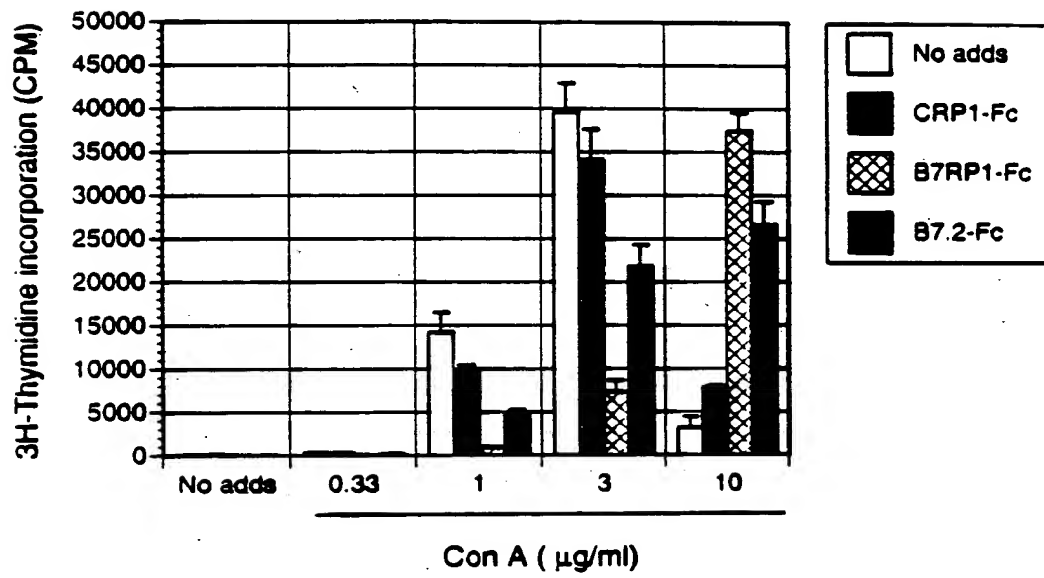


Figure 10

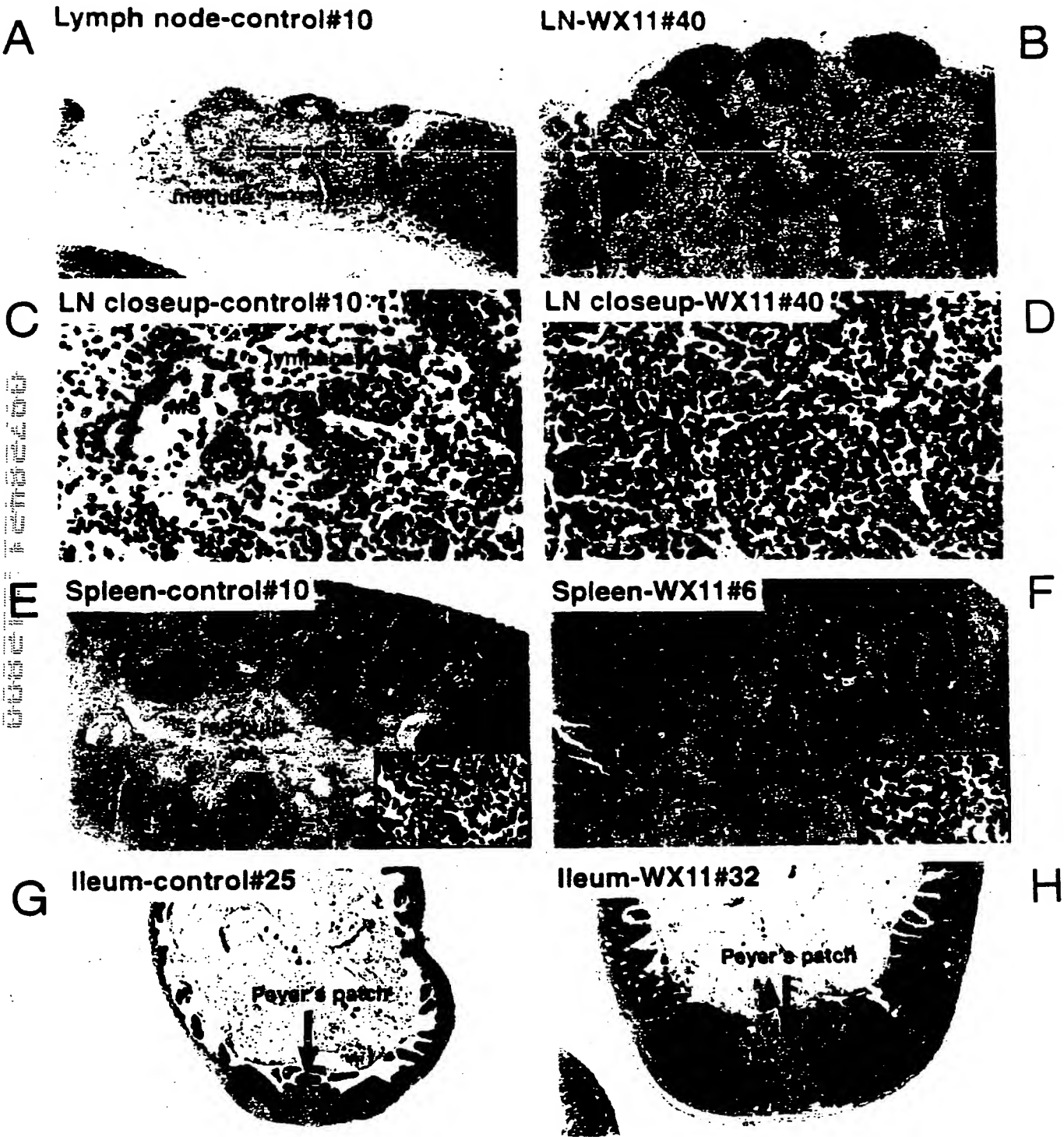


Figure 11

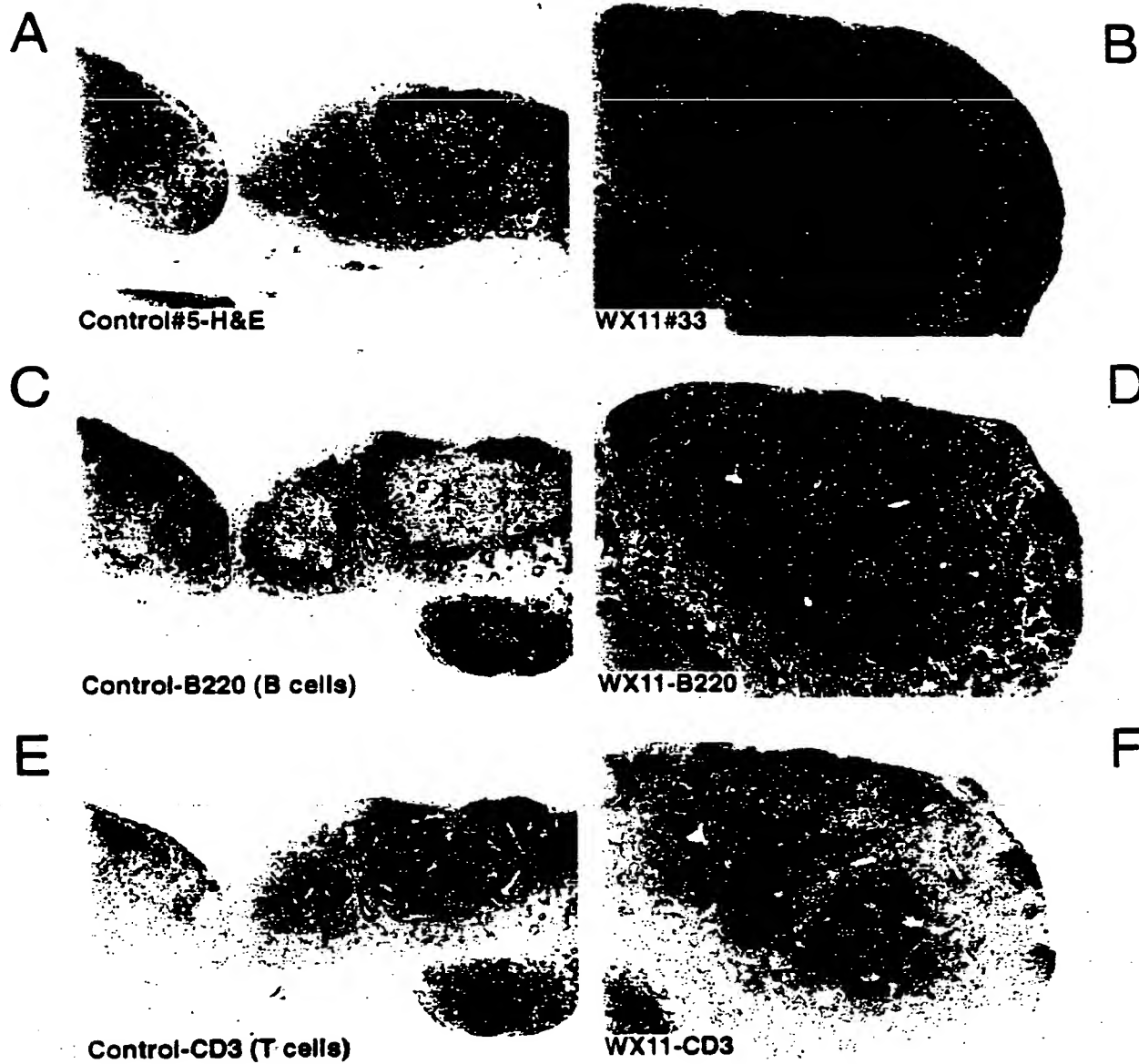


Figure 12A.

GCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCGCCCACGCG	-138
TCCGCGGGAGCGCAGTTAGAGCCGATCTCCCGCGCCCCGAGGTTGCTCCTCTCCGAGGTCTC	-75
CCGCGGCCCCAAGTTCTCCGCGCCCCGAGGTCTCCGCGCCCCGAGGTCTCCGCGGCCCCGAGGT	-14
CTCCGCCCCGACC	-1
ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC	45
M R L G S P G L L F L L F S S	
5 10 15	
CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC	90
L R A *D *T *Q *E K *E V R A *M V G	
20 25 30	
AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT	135
S D V E L S C A C P E G S R F	
35 40 45	
GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA	180
D L N D V Y V Y W Q T S E S K	
50 55 60	
ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC	225
T V V T Y H I P Q N S S L E N	
65 70 75	
GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC	270
V D S R Y R N R A L M S P A G	
80 85 90	
ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC	315
M L R G D F S L R L F N V T P	
95 100 105	
CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG	360
Q D E Q K F H C L V L S Q S L	
110 115 120	
GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA	405
G F Q E V L S V E V T L H V A	
125 130 135	
GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC	450
A N F S V P V V S A P H S P S	
140 145 150	
CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC	495
Q D E L T F T C T S I N G Y P	
155 160 165	
AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG	540
R P N V Y W I N K T D N S L L	
170 175 180	
GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC	585
D Q A L Q N D T V F L N M R G	
185 190 195	
TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC	630
L Y D V V S V L R I A R T P S	
200 205 210	
GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC	675
V N I G C C I E N V L L Q Q N	
215 220 225	

CTG	ACT	GTC	GGC	AGC	CAG	ACA	GGA	AAT	GAC	ATC	GGA	GAG	AGA	GAC	720
L	T	V	G	S	Q	T	G	N	D	I	G	E	R	D	
				230					235					240	
AAG	ATC	ACA	GAG	AAT	CCA	GTC	AGT	ACC	GGC	GAG	AAA	AAC	GCG	GCC	765
K	I	T	E	N	P	V	S	T	G	E	K	N	A	A	
				245					250					255	
ACG	TGG	AGC	ATC	CTG	GCT	GTC	CTG	TGC	CTG	CTT	GTG	GTC	GTG	GCG	810
T	W	S	I	L	A	V	L	C	L	L	V	V	V	A	
				260					265					270	
GTG	GCC	ATA	GGC	TGG	GTG	TGC	AGG	GAC	CGA	TGC	CTC	CAA	CAC	AGC	855
V	A	I	G	W	V	C	R	D	R	C	L	Q	H	S	
				275					280					285	
TAT	GCA	GGT	GCC	TGG	GCT	GTG	AGT	CCG	GAG	ACA	GAG	CTC	ACT	GGC	900
Y	A	G	A	W	A	V	S	P	E	T	E	L	T	G	
														300	
CAC	GTT	TGA													909
H	V	STOP													
		302													
CCGGAGCTC	ACCGCCC	CAGAGCGT	GACAGGGCTT	CCGTGAGAC	GCCACCGT	GAGAGGCC	CAGG								971
TGGCAGCTT	GAGCATG	GACTCCC	CAGACTGC	AGGGGAGC	ACTTGGGGC	CAGCCCC	CAGAAGGAC								1033
CACTGCTGGAT	CCCAGGG	GAGAACCT	GC	TGGCGTT	TGGCTGT	GATCCT	GGAATGAGG	CCCTTTC							1095

Figure 12B.

human	MRLGSP----	-----	-----G	L-LF-LLFSS	LRADTQEKEV	25
mouse	MLKPCPCFVS	LGTRQPWKK	LHVSSGFFSG	LGLFLLLSS	LCAASAETEV	50
Consensus	M.L..P....G	L.LF.LL.SS	L.A...E.EV	50
human	RAMVGSDEL	SCACPEGSRF	DLNDVYVWQ	TSESKTVVTV	HIPQNSSLEN	75
mouse	GAMVGSNVVL	SCIDPHRRHF	NLSGLYVWQ	IENPEVSVTV	YLPYKSPGIN	100
Consensus	.AMVGS.V.L	SC..P....F	.L...YVWQVTY	..P..S...N	100
human	VDSRYRNRAL	MSPAGMLRGD	FSLRLFNVTP	QDEQKFHCLV	LSQ-SLGFQE	124
mouse	VDSSYKNRGH	LSLDSMKQGN	FSLYLKNVTP	QDTQEFTCRV	FMNTATELVK	150
Consensus	VDS.Y.NR..	.S...M..G.	FSL.L.NVTP	QD.Q.F.C.V	150
human	VLSVEVTLHV	AANFSVPVVS	APHSPSQ-DE	LTFTCTSING	YPRPNVYWIN	173
mouse	ILEEVRLRV	AANFSTPVIS	TSDSSNPGQE	RTYTCMSKNG	YPEPNLYWIN	200
Consensus	.L...V.L.V	AANFS.PV.S	...S.....E	.T.TC.S.NG	YP.PN.YWIN	200
human	KTDNSLLDQA	LQNDTVFLNM	RGLYDVVSVL	RIARTPSVNI	GCCIENTVLLQ	223
mouse	TTDNSLIDTA	LQNNTVYLNK	LGLYDVISTL	RLPWTSRGDV	LCCVENVALH	250
Consensus	.TDNSL.D.A	LQN.TV.LN.	.GLYDV.S.L	R...T.....	.CC.ENV.L.	250
human	QNLTVGSQTG	NDIGERDKIT	ENPVSTGEKN	AATWSILAVL	CLLVVVAVAI	273
mouse	QNITSISQAE	SFTGNNTKNP	QETHNNELKV	LV--PVLAVL	AAAAFVSFII	298
Consensus	QN.T..SQ..	...G...K..K.LAVLV...I	300
human	GWVCRDRCLQ	HSYAGAWAVS	PETELTGHV			302
mouse	YR--RTR-PH	RSYTGPKTVQ	LE--LTDHA			322
ConsensusR.R...	.SY.G...V.	.E..LT.H.			329

Figure 13A

AACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCTAATACGA
 CTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTC
 GACCCACGCGTCCGTGAACACTGAACGCGAGGACTGTAACTGTTTCTGGCAAAC

ATG AAG TCA GGC CTC TGG TAT TTC TTT CTC TTC TGC TTG CGC ATT 45
 M K S G L W Y F F L F C L R I
 5 10 15

AAA GTT TTA ACA GGA GAA ATC AAT GGT TCT GCC AAT TAT GAG ATG 90
 K V L T *G *E I N G S A N Y E M
 20 25 30

TTT ATA TTT CAC AAC GGA GGT GTA CAA ATT TTA TGC AAA TAT CCT 135
 F I F H N G G V Q I L C K Y P
 35 40 45

GAC ATT GTC CAG CAA TTT AAA ATG CAG TTG CTG AAA GGG GGG CAA 180
 D I V Q Q F K M Q L L K G G Q
 50 55 60

ATA CTC TGC GAT CTC ACT AAG ACA AAA GGA AGT GGA AAC ACA GTG 225
 I L C D L T K T K G S G N T V
 65 70 75

TCC ATT AAG AGT CTG AAA TTC TGC CAT TCT CAG TTA TCC AAC AAC 270
 S I K S L K F C H S Q L S N N
 80 85 90

AGT GTC TCT TTT TTT CTA TAC AAC TTG GAC CAT TCT CAT GCC AAC 315
 S V S F F L Y N L D H S H A N
 95 100 105

TAT TAC TTC TGC AAC CTA TCA ATT TTT GAT CCT CCT CCT TTT AAA 360
 Y Y F C N L S I F D P P P F K
 110 115 120

GTA ACT CTT ACA GGA GGA TAT TTG CAT ATT TAT GAA TCA CAA CTT 405
 V T L T G G Y L H I Y E S Q L
 125 130 135

TGT TGC CAG CTG AAG TTC TGG TTA CCC ATA GGA TGT GCA GCC TTT 450
 C C Q L K F W L P I G C A A F
 140 145 150

GTT GTA GTC TGC ATT TTG GGA TGC ATA CTT ATT TGT TGG CTT ACA 495
 V V V C I L G C I L I C W L T
 155 160 165

AAA AAG AAG TAT TCA TCC AGT GTG CAC GAC CCT AAC GGT GAA TAC 540
 K K K Y S S S V H D P N G E Y
 170 175 180

ATG TTC ATG AGA GCA GTG AAC ACA GCC AAA AAA TCT AGA CTC ACA 585
 M F M R A V N T A K K S R L T
 185 190 195

GAT GTG ACC CTA TAA 600
 D V T L STOP
 199

TATGGAACCTCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTTCTCAACTTGA 655
 AGTGCAAGATTCTCTTATTTCGGGACCACGGAGAGTCTGACTTAACATACATA 710

Figure 13B

hCRP1	MKSGWLWYFFLFCLRIKVL TGEINGSANYEMFIFHNGGVQILCKYPDIVQQ	50
mCRP1	. :. .:. : MKPYFCRVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQQ	50
hCRP1	FKMQLLKGGQILCDLTKTKGSGNTVSIKSLKFCHSQLSNNSVSFFLYNLD	100
mCRP1	. : :. . LKMRLFREREVLCELTCTKGSGNAVS IKNPMLCLYHLSNNSVSFFLNND	100
hCRP1	HSNANYFCNLSIFDPPPFKV.TLTGGYLHIYESQLCCQLKFWLPVIGCAA	149
mCRP1	. . . : SSQGSYYFCSLSIFDPPPFQERNLSGGYLHIYESQLCCQLKLWLPVGCAA	150
hCRP1	FVVVCILGCILICWLTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL	199
mCRP1	: . FVVVLLFGCILIIWFSKKKYGSSVHDPNSEYMFMAAVNTNKKSLAGVTS	200

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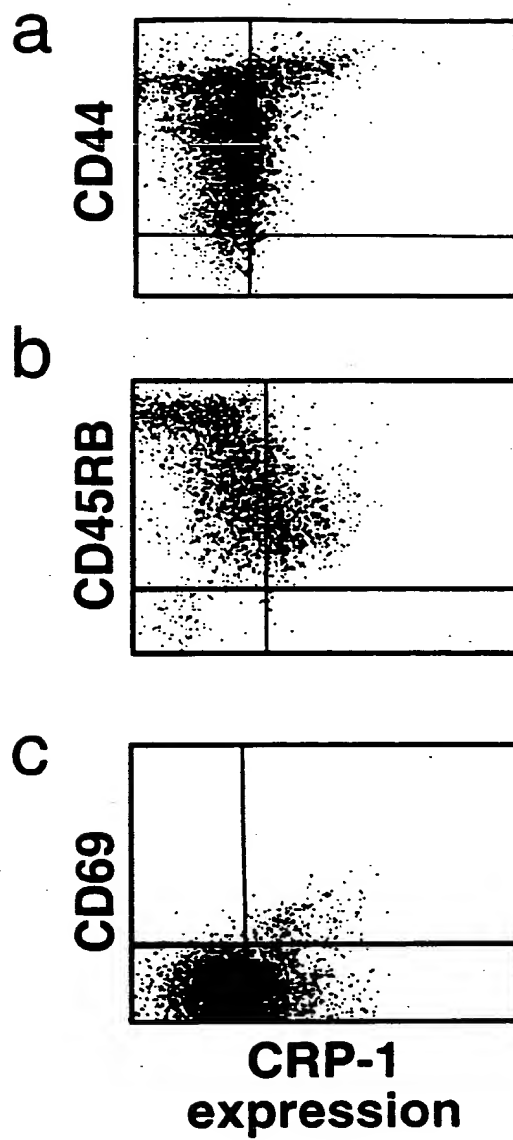
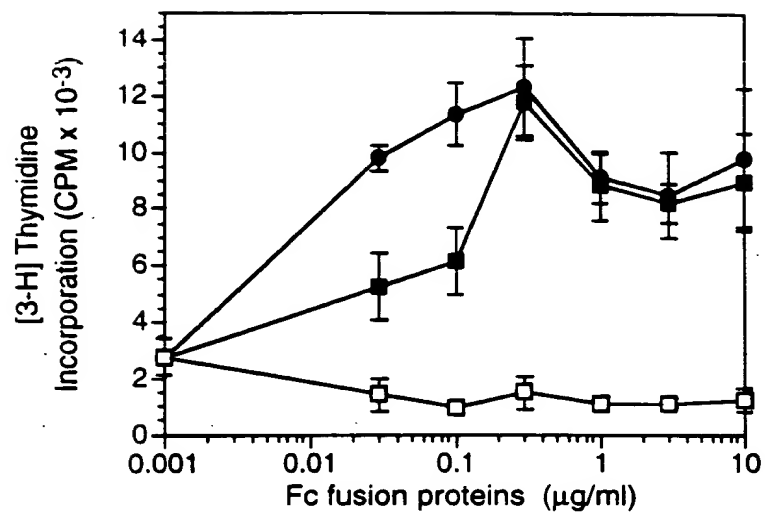


Figure 14

a



b

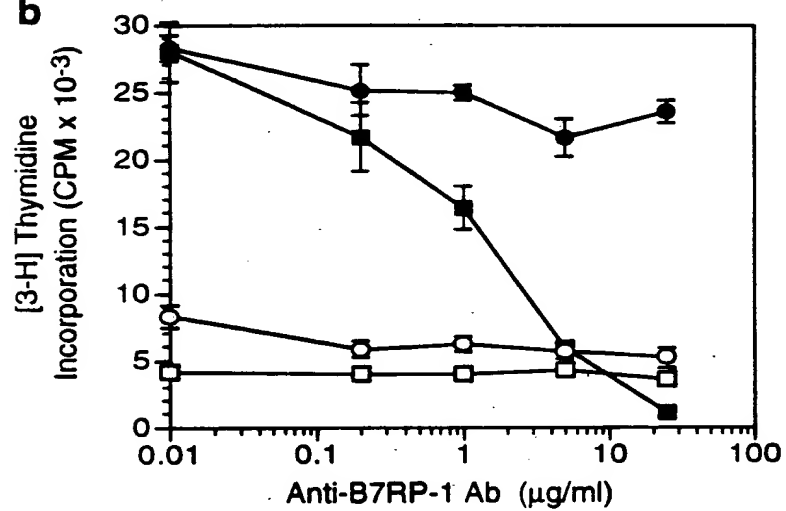
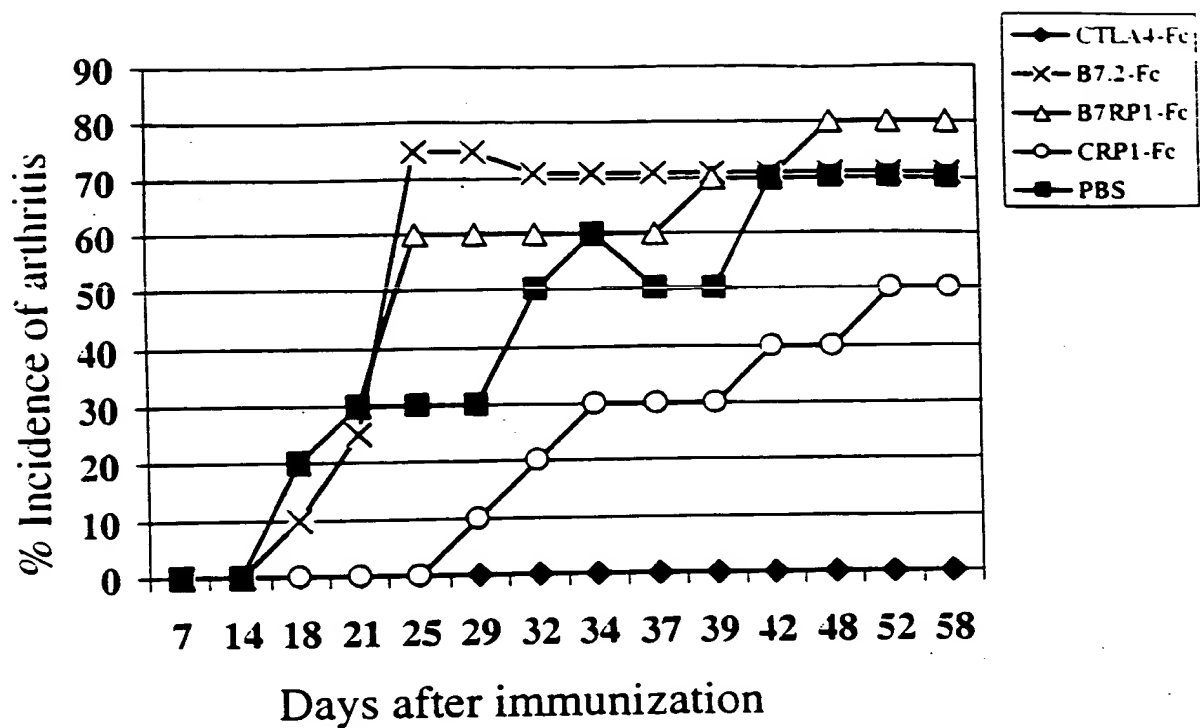


Figure 15

A.



B.

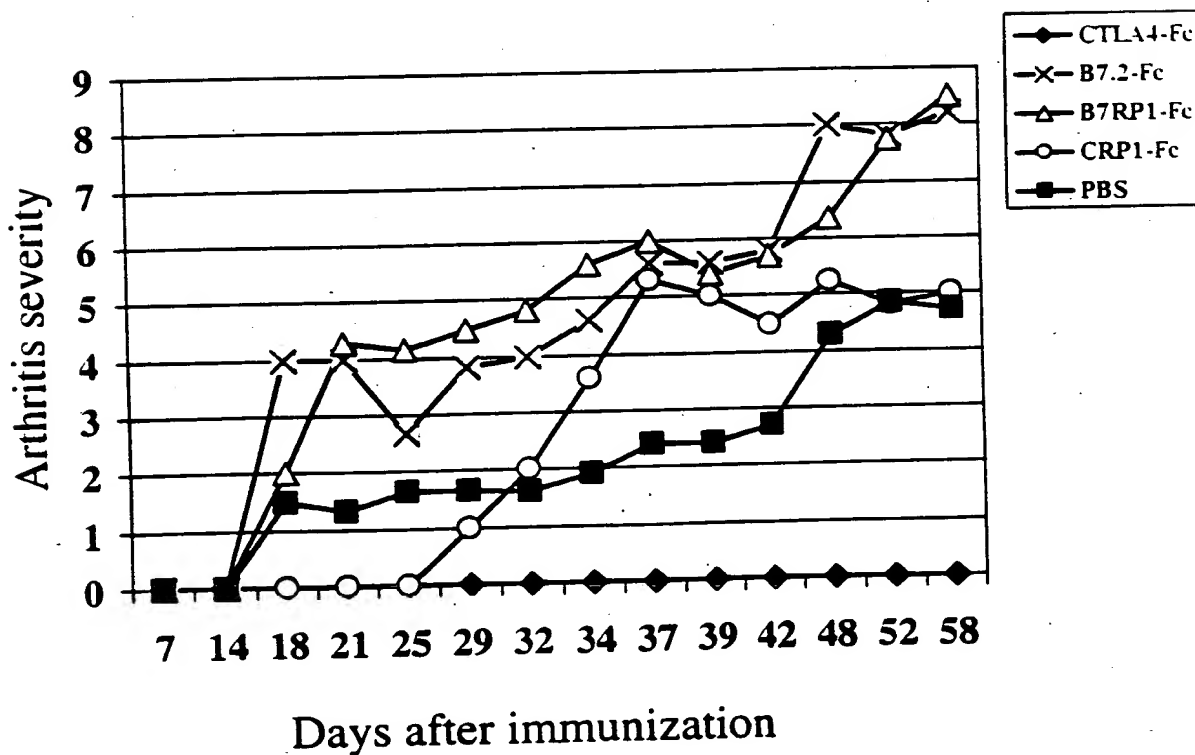
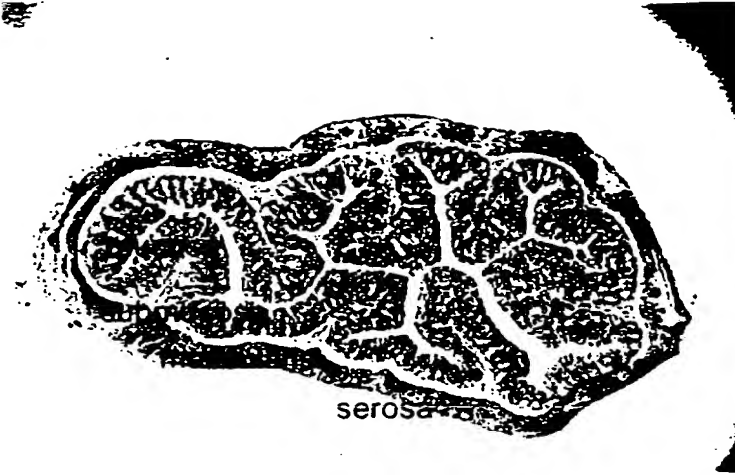
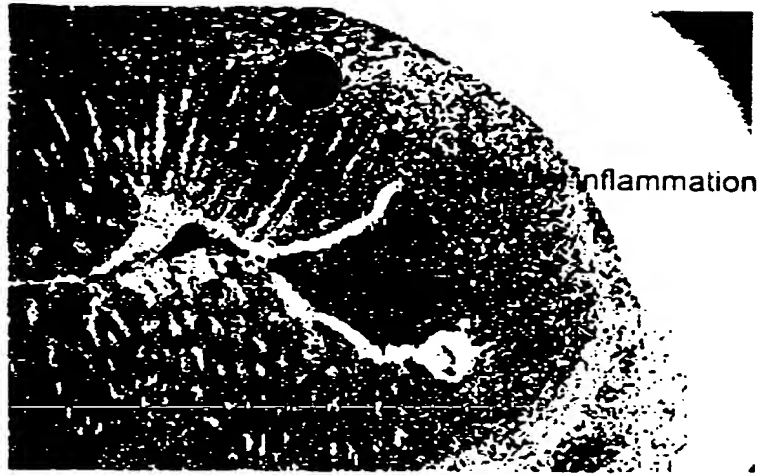


Figure 16



A. Control mouse#53F:Prox. colon 40X



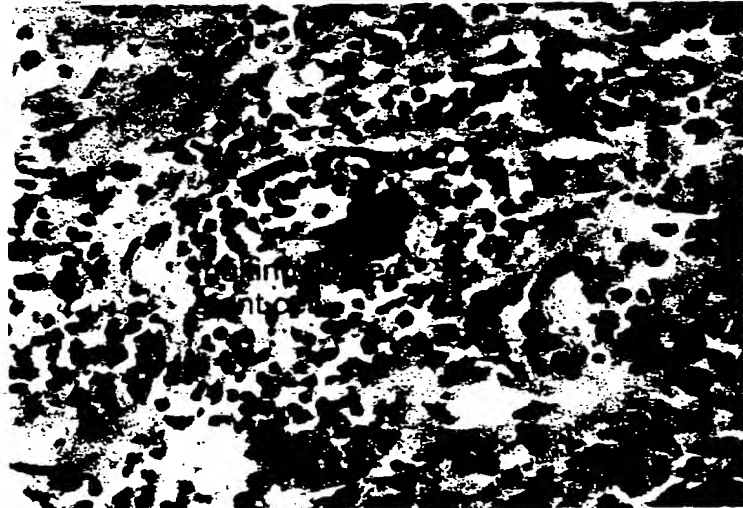
B. Mouse#111F:Prox. colon 40X



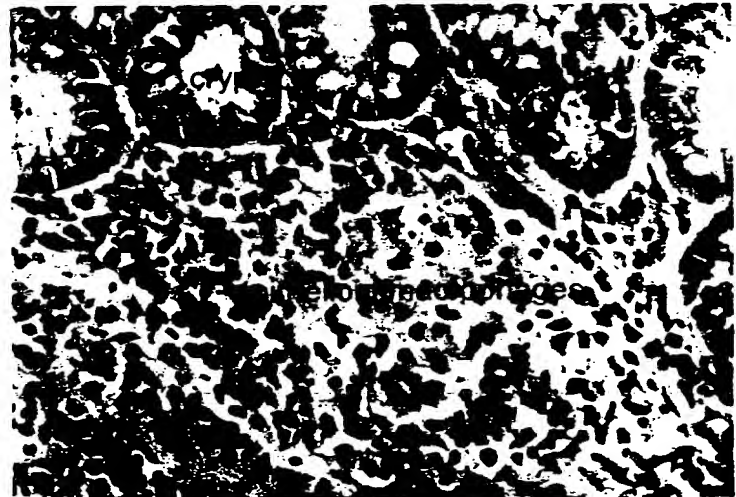
C. Mouse#111F: Prox. colon 20X



D. Mouse#111F: closeup of mucosa 100X

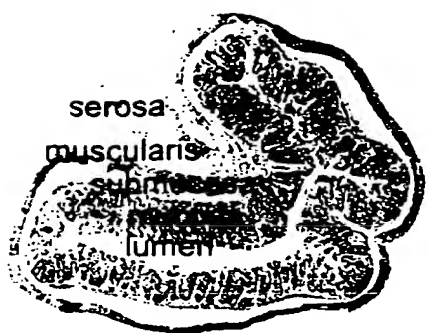


E. Mouse#112F: Giant cell, submucosa

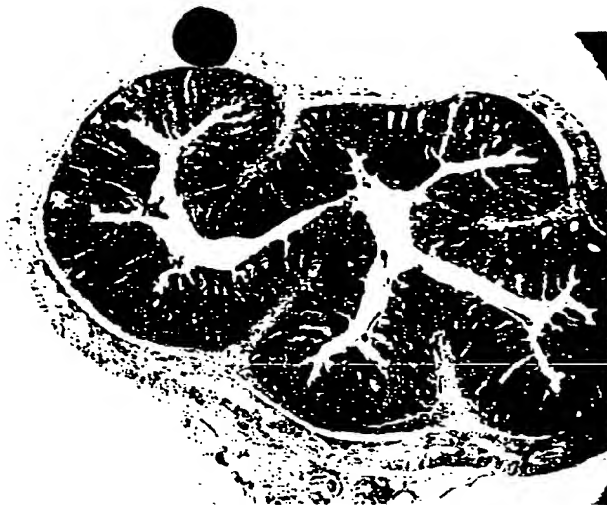


F. Mouse#112F:epithelioid macrophages

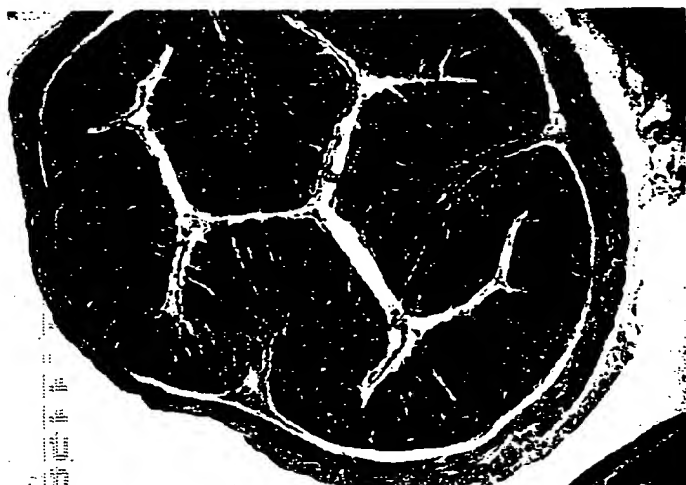
Figure 17



A. Control mouse#53F:Distal colon, 40X



B. mouse#111F:Distal colitis, 40X



C. mouse#55M:Distal colitis, 40X



D. mouse#112F:Distal colon, 40X

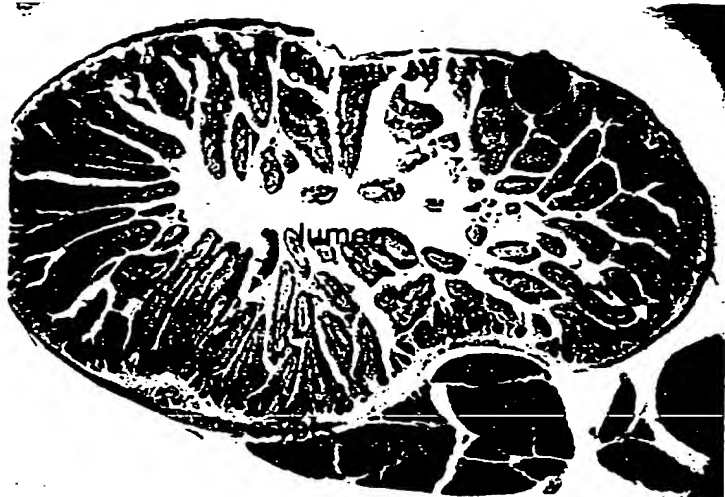


E. mouse#112:CD3+ T-cells, 40X



F. mouse#112:closeup, 100X

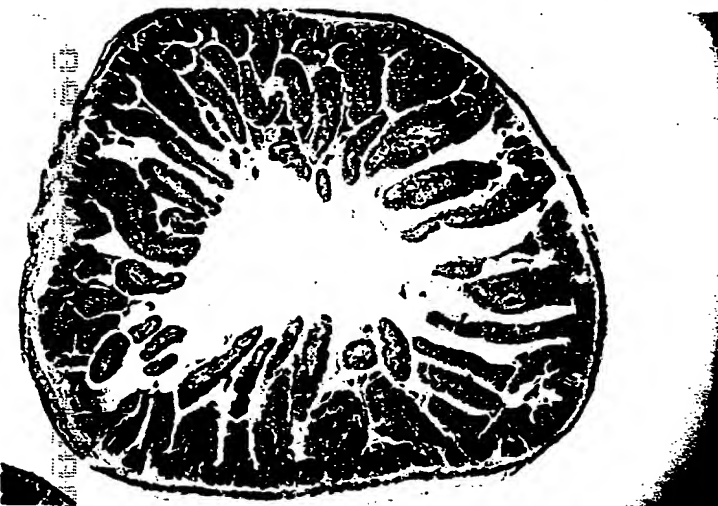
Figure 18



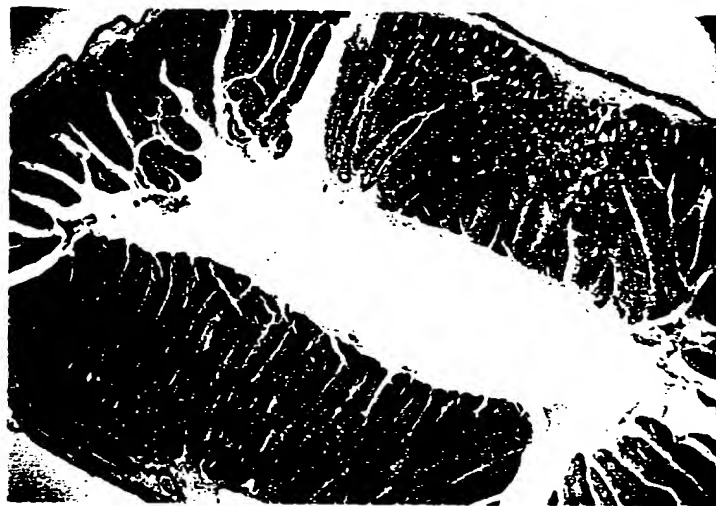
A. Control mouse#53F:duodenum, 40X



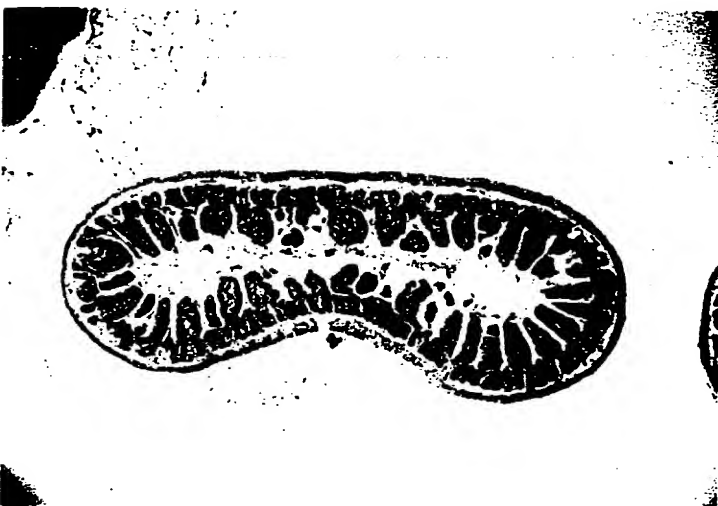
B. Mouse#51F:duodenum, 40X



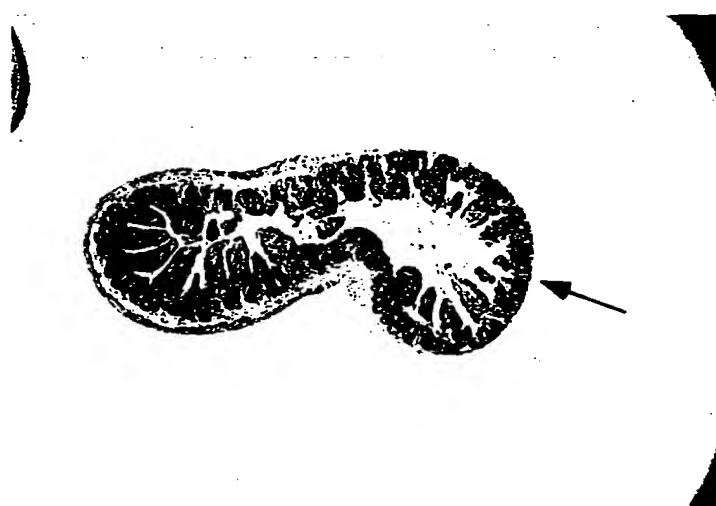
C. Control mouse#53F:jejunum, 40X



D. Mouse#51F:jejunal hyperplasia, 40X



E. Control mouse#53F:ileum, 40X



F. Mouse#231M:ileal atrophy, 40X

Figure 19

Figure 20

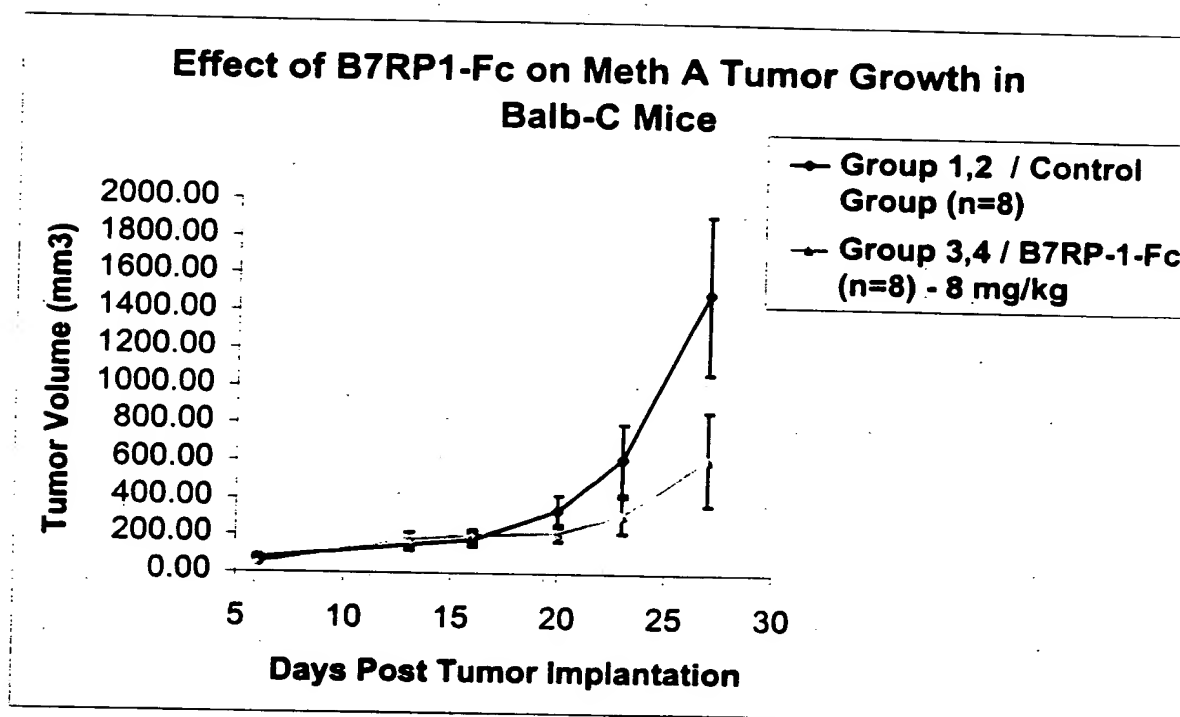


Figure 21A/B.

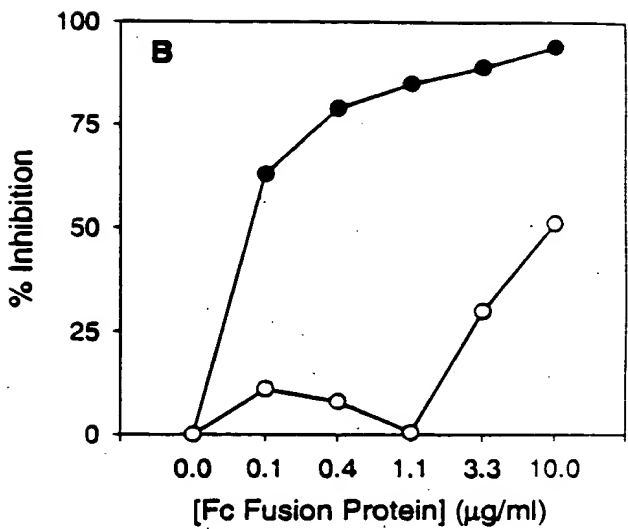
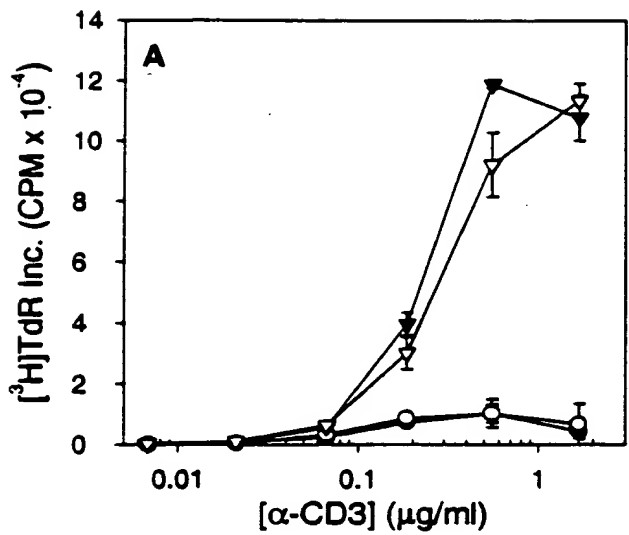


Figure 21C.

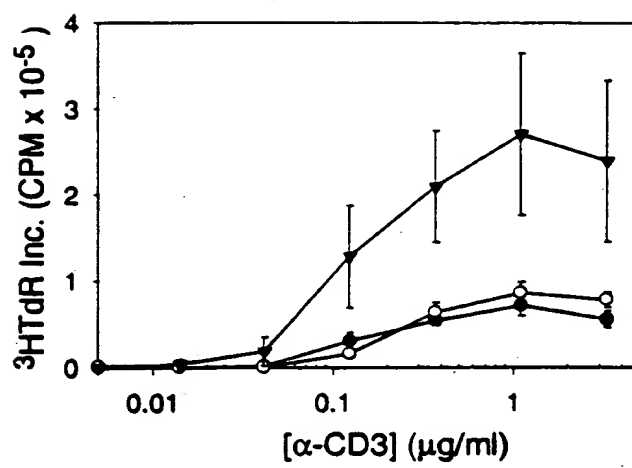


Figure 21D

